

Sequence Listing

<110> Kureha Chemical Industry Co., Ltd.

<120> Novel Proteins and Novel Genes Encoding the Same

<130> KRH-647

<150> JP 2000-042933

<151> 2000-02-21

<160> 10

<210> 1

<211> 2180

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (37)..(1482)

<400> 1

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                               1           5

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Thr Glu Ser Phe Ala Thr Ala Ile His Gly Leu Lys Val Gly His Leu
      10           15           20

aca gat cgt gtt att cag agg agc aag agg atg att cta gac act ctg   150
Thr Asp Arg Val Ile Gln Arg Ser Lys Arg Met Ile Leu Asp Thr Leu
      25           30           35

ggc gct ggg ttc ctg gga acc act acg gaa gtg ttt cac ata gcc agc   198
Gly Ala Gly Phe Leu Gly Thr Thr Thr Glu Val Phe His Ile Ala Ser
      40           45           50

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caa tat agc aag atc tac agt tcc aac ata tcc agc act gta tgg ggt	246
Gln Tyr Ser Lys Ile Tyr Ser Ser Asn Ile Ser Ser Thr Val Trp Gly	
55 60 65 70	
cag cca gac atc agg ctc ccg ccc aca tat gct gct ttt gtg aac ggt	294
Gln Pro Asp Ile Arg Leu Pro Pro Thr Tyr Ala Ala Phe Val Asn Gly	
75 80 85	
gtg gct att cac tcc atg gat ttt gat gac acg tgg cac cct gcc acc	342
Val Ala Ile His Ser Met Asp Phe Asp Asp Thr Trp His Pro Ala Thr	
90 95 100	
cac cct tct ggg gct gtc ctt cct gtc ctc aca gct tta gca gaa gcc	390
His Pro Ser Gly Ala Val Leu Pro Val Leu Thr Ala Leu Ala Glu Ala	
105 110 115	
ctg cca agg agt cca aag ttt tct ggc ctt gac ctg ctg ctg gct ttc	438
Leu Pro Arg Ser Pro Lys Phe Ser Gly Leu Asp Leu Leu Leu Ala Phe	
120 125 130	
aat gtt ggt att gaa gtg caa ggc cga tta ctg cat ttc gcc aag gag	486
Asn Val Gly Ile Glu Val Gln Gly Arg Leu Leu His Phe Ala Lys Glu	
135 140 145 150	
gcc aat gac atg cca aag aga ttc cat ccc cct tcc gtg gta gga acg	534
Ala Asn Asp Met Pro Lys Arg Phe His Pro Pro Ser Val Val Gly Thr	
155 160 165	
ttg ggt agt gct gct gct gca tcc aag ttt tta gga ctt agc tcg aca	582
Leu Gly Ser Ala Ala Ala Ala Ser Lys Phe Leu Gly Leu Ser Ser Thr	
170 175 180	
aag tgc cga gaa gct ctg gcc att gct gtt tcc cat gct ggg gca ccc	630
Lys Cys Arg Glu Ala Leu Ala Ile Ala Val Ser His Ala Gly Ala Pro	
185 190 195	
atg gcc aat gct gcc acc cag acc aag ccc ctc cac att ggc aat gct	678

Met	Ala	Asn	Ala	Ala	Thr	Gln	Thr	Lys	Pro	Leu	His	Ile	Gly	Asn	Ala		
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gcc aag cat ggg ata gaa gct gca ttt ttg gca atg ttg ggt ctc caa 726																	
Ala Lys His Gly Ile Glu Ala Ala Phe Leu Ala Met Leu Gly Leu Gln																	
215						220				225					230		
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Gly Asn Lys Gln Val Leu Asp Leu Glu Ala Gly Phe Gly Ala Phe Tyr																	
				235				240					245				
gcc aac tat tcc cca aaa gtc ctt cca agc ata gct tcc tac agt tgg 822																	
Ala Asn Tyr Ser Pro Lys Val Leu Pro Ser Ile Ala Ser Tyr Ser Trp																	
			250					255					260				
ctg ctg gac cag cag gac gtg gcc ttt aag cgt ttt cct gca cat tta 870																	
Leu Leu Asp Gln Gln Asp Val Ala Phe Lys Arg Phe Pro Ala His Leu																	
			265					270					275				
tct acc cac tgg gtg gca gac gca gct gca tct gtg aga aag cac ctt 918																	
Ser Thr His Trp Val Ala Asp Ala Ala Ala Ser Val Arg Lys His Leu																	
			280					285					290				
gta gca gag aga gcc ctg ctt cca act gac tac att aag aga att gtg 966																	
Val Ala Glu Arg Ala Leu Leu Pro Thr Asp Tyr Ile Lys Arg Ile Val																	
295						300				305					310		
ctc agg ata cca aat gtc cag tat gta aac agg ccc ttt cca gtt tcg 1014																	
Leu Arg Ile Pro Asn Val Gln Tyr Val Asn Arg Pro Phe Pro Val Ser																	
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gag cat gaa gcc cgt cat tca ttc cag tat gtg gcc tgt gcc atg ctg 1062																	
Glu His Glu Ala Arg His Ser Phe Gln Tyr Val Ala Cys Ala Met Leu																	
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ctt gat ggt ggc atc act gtc ccc tca ttc cat gaa tgc cag atc aac 1110																	
Leu Asp Gly Gly Ile Thr Val Pro Ser Phe His Glu Cys Gln Ile Asn																	
			345					350					355				

agg cca cag gtg aga gag ctg ctc agt aag gtg gag ctg gag tac cct 1158
 Arg Pro Gln Val Arg Glu Leu Leu Ser Lys Val Glu Leu Glu Tyr Pro
 360 365 370

ccg gac aac ttg cca agc ttc aac ata ctg tac tgt gaa ata agt gtc 1206
 Pro Asp Asn Leu Pro Ser Phe Asn Ile Leu Tyr Cys Glu Ile Ser Val
 375 380 385 390

acc ctc aag gat gga gcc acc ttc aca gat cgc tct gat acc ttc tat 1254
 Thr Leu Lys Asp Gly Ala Thr Phe Thr Asp Arg Ser Asp Thr Phe Tyr
 395 400 405

ggg cac tgg aga aaa cca ctg agc cag gag gac cta gag gaa aag ttc 1302
 Gly His Trp Arg Lys Pro Leu Ser Gln Glu Asp Leu Glu Glu Lys Phe
 410 415 420

aga gcc aat gcc tcc aag atg ctg tcc tgg gac aca gtg gaa agc ctt 1350
 Arg Ala Asn Ala Ser Lys Met Leu Ser Trp Asp Thr Val Glu Ser Leu
 425 430 435

ata aag ata gtc aaa aat cta gaa gac cta gaa gac tgt tct gtg tta 1398
 Ile Lys Ile Val Lys Asn Leu Glu Asp Leu Glu Asp Cys Ser Val Leu
 440 445 450

act aca ctt ctc aaa gga ccc tct cca cca gag gta gct tca aac tct 1446
 Thr Thr Leu Leu Lys Gly Pro Ser Pro Pro Glu Val Ala Ser Asn Ser
 455 460 465 470

cca gca tgt aat aat tct atc aca aat ctc tcc tgaggcttac caacatctaa 1499
 Pro Ala Cys Asn Asn Ser Ile Thr Asn Leu Ser
 475 480

atgactttgc atttggggag attcaatgat ttggtttgta aagcaagggt ctgctgcttg 1559

gttttcccag gaaaaatgaa caaagatgga gagagtccag aaacagaact acatatatct 1619

ggaaggagcc ttctcctgaa aattttgcag gacagttcca cttacctaaa tcaagatgaa 1679

acacacacac aaaaatgagt ttgtaagcat tcacaagggt gaaattcaac tcacctgtga 1739
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 agtctggaaa aatcgcatit ttggtctaga acccatggtc ttaagcactg caatatatca 2099
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 aagtaaaaaa aaaaaaaaaa a 2180

<210> 2

<211> 481

<212> PRT

<213> Homo sapiens

<400> 2

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1 5 10 15

Leu Lys Val Gly His Leu Thr Asp Arg Val Ile Gln Arg Ser Lys Arg

20 25 30

Met Ile Leu Asp Thr Leu Gly Ala Gly Phe Leu Gly Thr Thr Thr Glu

35 40 45

Val Phe His Ile Ala Ser Gln Tyr Ser Lys Ile Tyr Ser Ser Asn Ile

50 55 60

Ser Ser Thr Val Trp Gly Gln Pro Asp Ile Arg Leu Pro Pro Thr Tyr
 65 70 75 80

Ala Ala Phe Val Asn Gly Val Ala Ile His Ser Met Asp Phe Asp Asp
 85 90 95

Thr Trp His Pro Ala Thr His Pro Ser Gly Ala Val Leu Pro Val Leu
 100 105 110

Thr Ala Leu Ala Glu Ala Leu Pro Arg Ser Pro Lys Phe Ser Gly Leu
 115 120 125

Asp Leu Leu Leu Ala Phe Asn Val Gly Ile Glu Val Gln Gly Arg Leu
 130 135 140

Leu His Phe Ala Lys Glu Ala Asn Asp Met Pro Lys Arg Phe His Pro
 145 150 155 160

Pro Ser Val Val Gly Thr Leu Gly Ser Ala Ala Ala Ala Ser Lys Phe
 165 170 175

Leu Gly Leu Ser Ser Thr Lys Cys Arg Glu Ala Leu Ala Ile Ala Val
 180 185 190

Ser His Ala Gly Ala Pro Met Ala Asn Ala Ala Thr Gln Thr Lys Pro
 195 200 205

Leu His Ile Gly Asn Ala Ala Lys His Gly Ile Glu Ala Ala Phe Leu
 210 215 220

Ala Met Leu Gly Leu Gln Gly Asn Lys Gln Val Leu Asp Leu Glu Ala
 225 230 235 240

Gly Phe Gly Ala Phe Tyr Ala Asn Tyr Ser Pro Lys Val Leu Pro Ser
 245 250 255

Ile Ala Ser Tyr Ser Trp Leu Leu Asp Gln Gln Asp Val Ala Phe Lys
 260 265 270

Arg Phe Pro Ala His Leu Ser Thr His Trp Val Ala Asp Ala Ala Ala
 275 280 285

Ser Val Arg Lys His Leu Val Ala Glu Arg Ala Leu Leu Pro Thr Asp
 290 295 300

Tyr Ile Lys Arg Ile Val Leu Arg Ile Pro Asn Val Gln Tyr Val Asn
 305 310 315 320

Arg Pro Phe Pro Val Ser Glu His Glu Ala Arg His Ser Phe Gln Tyr
 325 330 335

Val Ala Cys Ala Met Leu Leu Asp Gly Gly Ile Thr Val Pro Ser Phe
 340 345 350

His Glu Cys Gln Ile Asn Arg Pro Gln Val Arg Glu Leu Leu Ser Lys
 355 360 365

Val Glu Leu Glu Tyr Pro Pro Asp Asn Leu Pro Ser Phe Asn Ile Leu
 370 375 380

Tyr Cys Glu Ile Ser Val Thr Leu Lys Asp Gly Ala Thr Phe Thr Asp
 385 390 395 400

Arg Ser Asp Thr Phe Tyr Gly His Trp Arg Lys Pro Leu Ser Gln Glu
 405 410 415

Asp Leu Glu Glu Lys Phe Arg Ala Asn Ala Ser Lys Met Leu Ser Trp
 420 425 430

Asp Thr Val Glu Ser Leu Ile Lys Ile Val Lys Asn Leu Glu Asp Leu
 435 440 445

Glu Asp Cys Ser Val Leu Thr Thr Leu Leu Lys Gly Pro Ser Pro Pro
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Glu Val Ala Ser Asn Ser Pro Ala Cys Asn Asn Ser Ile Thr Asn Leu

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470

475

480

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<211> 1970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (126)..(1298)

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actcc atg gat ttt gat gac acg tgg cac cct gcc acc cac cct tct ggg 170

Met Asp Phe Asp Asp Thr Trp His Pro Ala Thr His Pro Ser Gly

1

5

10

15

gct gtc ctt cct gtc ctc aca gct tta gca gaa gcc ctg cca agg agt 218

Ala Val Leu Pro Val Leu Thr Ala Leu Ala Glu Ala Leu Pro Arg Ser

20

25

30

cca aag ttt tct ggc ctt gac ctg ctg ctg gct ttc aat gtt ggt att 266

Pro Lys Phe Ser Gly Leu Asp Leu Leu Leu Ala Phe Asn Val Gly Ile

35

40

45

gaa gtg caa ggc cga tta ctg cat ttc gcc aag gag gcc aat gac atg 314

Glu Val Gln Gly Arg Leu Leu His Phe Ala Lys Glu Ala Asn Asp Met

50

55

60

cca aag aga ttc cat ccc cct tcc gtg gta gga acg ttg ggt agt gct 362

Pro Lys Arg Phe His Pro Pro Ser Val Val Gly Thr Leu Gly Ser Ala

65

70

75

gct gct gca tcc aag ttt tta gga ctt agc tcg aca aag tgc cga gaa	410
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80 85 90 95	
gct ctg gcc att gct gtt tcc cat gct ggg gca ccc atg gcc aat gct	458
Ala Leu Ala Ile Ala Val Ser His Ala Gly Ala Pro Met Ala Asn Ala	
100 105 110	
gcc acc cag acc aag ccc ctc cac att ggc aat gct gcc aag cat ggg	506
Ala Thr Gln Thr Lys Pro Leu His Ile Gly Asn Ala Ala Lys His Gly	
115 120 125	
ata gaa gct gca ttt ttg gca atg ttg ggt ctc caa gga aac aag cag	554
Ile Glu Ala Ala Phe Leu Ala Met Leu Gly Leu Gln Gly Asn Lys Gln	
130 135 140	
gtc ttg gac ttg gag gca gga ttt ggg gcc ttt tat gcc aac tat tcc	602
Val Leu Asp Leu Glu Ala Gly Phe Gly Ala Phe Tyr Ala Asn Tyr Ser	
145 150 155	
cca aaa gtc ctt cca agc ata gct tcc tac agt tgg ctg ctg gac cag	650
Pro Lys Val Leu Pro Ser Ile Ala Ser Tyr Ser Trp Leu Leu Asp Gln	
160 165 170 175	
cag gac gtg gcc ttt aag cgt ttt cct gca cat tta tct acc cac tgg	698
Gln Asp Val Ala Phe Lys Arg Phe Pro Ala His Leu Ser Thr His Trp	
180 185 190	
gtg gca gac gca gct gca tct gtg aga aag cac ctt gta gca gag aga	746
Val Ala Asp Ala Ala Ala Ser Val Arg Lys His Leu Val Ala Glu Arg	
195 200 205	
gcc ctg ctt cca act gac tac att aag aga att gtg ctc agg ata cca	794
Ala Leu Leu Pro Thr Asp Tyr Ile Lys Arg Ile Val Leu Arg Ile Pro	
210 215 220	
aat gtc cag tat gta aac agg ccc ttt cca gtt tcg gag cat gaa gcc	842

Asn Val Gln Tyr Val Asn Arg Pro Phe Pro Val Ser Glu His Glu Ala	
225 230 235	
cg t cat tca ttc cag tat gtg gcc tgt gcc atg ctg ctt gat ggt ggc	890
Arg His Ser Phe Gln Tyr Val Ala Cys Ala Met Leu Leu Asp Gly Gly	
240 245 250 255	
atc act gtc ccc tca ttc cat gaa tgc cag atc aac agg cca cag gtg	938
Ile Thr Val Pro Ser Phe His Glu Cys Gln Ile Asn Arg Pro Gln Val	
260 265 270	
aga gag ctg ctc agt aag gtg gag ctg gag tac cct ccg gac aac ttg	986
Arg Glu Leu Leu Ser Lys Val Glu Leu Glu Tyr Pro Pro Asp Asn Leu	
275 280 285	
cca agc ttc aac ata ctg tac tgt gaa ata agt gtc acc ctc aag gat	1034
Pro Ser Phe Asn Ile Leu Tyr Cys Glu Ile Ser Val Thr Leu Lys Asp	
290 295 300	
gga gcc acc ttc aca gat cgc tct gat acc ttc tat ggg cac tgg aga	1082
Gly Ala Thr Phe Thr Asp Arg Ser Asp Thr Phe Tyr Gly His Trp Arg	
305 310 315	
aaa cca ctg agc cag gag gac cta gag gaa aag ttc aga gcc aat gcc	1130
Lys Pro Leu Ser Gln Glu Asp Leu Glu Glu Lys Phe Arg Ala Asn Ala	
320 325 330 335	
tcc aag atg ctg tcc tgg gac aca gtg gaa agc ctt ata aag ata gtc	1178
Ser Lys Met Leu Ser Trp Asp Thr Val Glu Ser Leu Ile Lys Ile Val	
340 345 350	
aaa aat cta gaa gac cta gaa gac tgt tct gtg tta act aca ctt ctc	1226
Lys Asn Leu Glu Asp Leu Glu Asp Cys Ser Val Leu Thr Thr Leu Leu	
355 360 365	
aaa gga ccc tct cca cca gag gta gct tca aac tct cca gca tgt aat	1274
Lys Gly Pro Ser Pro Pro Glu Val Ala Ser Asn Ser Pro Ala Cys Asn	
370 375 380	

aat tct atc aca aat ctc tcc tgaggcttac caacatctaa atgactttgc 1325

Asn Ser Ile Thr Asn Leu Ser

385

390

atttggggag attcaatgat ttggtttgta aagcaagggt ctgctgcttg gttttcccag 1385

gaaaaatgaa caaagatgga gagagtccag aaacagaact acatatatct ggaaggagcc 1445

ttctcctgaa aattttgcag gacagttcca cttacctaaa tcaagatgaa acacacacac 1505

aaaaatgagt ttgtaagcat tcacaagggt gaaattcaac tcacctgtga ttactttata 1565

aaattaatct cttcatagga attatgtgtg gacttcatga gcctcaagggt tttagaggga 1625

tgatgaacctg catgtatatt ttctgacagt ggagaggggt ctggtgcatt gtgtcaccaa 1685

cagatctcct agaccatggc ttattaccaa gccctccaca gtgcaagggg tgctactggg 1745

gaatgggtgg gtttaaatcc tgcctctgcc attcactaga ttagccttg agcatgttac 1805

cattagccct ctgcctcagt ttccctatit gtcaagccga agtaaaaagc agtctggaaa 1865

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<210> 4

<211> 390

<212> PRT

<213> Homo sapiens

<400> 4

Met Asp Phe Asp Asp Thr Trp His Pro Ala Thr His Pro Ser Gly Ala

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5

10

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Val Leu Pro Val Leu Thr Ala Leu Ala Glu Ala Leu Pro Arg Ser Pro

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Lys Phe Ser Gly Leu Asp Leu Leu Leu Ala Phe Asn Val Gly Ile Glu		
35	40	45
Val Gln Gly Arg Leu Leu His Phe Ala Lys Glu Ala Asn Asp Met Pro		
50	55	60
Lys Arg Phe His Pro Pro Ser Val Val Gly Thr Leu Gly Ser Ala Ala		
65	70	75 80
Ala Ala Ser Lys Phe Leu Gly Leu Ser Ser Thr Lys Cys Arg Glu Ala		
85	90	95
Leu Ala Ile Ala Val Ser His Ala Gly Ala Pro Met Ala Asn Ala Ala		
100	105	110
Thr Gln Thr Lys Pro Leu His Ile Gly Asn Ala Ala Lys His Gly Ile		
115	120	125
Glu Ala Ala Phe Leu Ala Met Leu Gly Leu Gln Gly Asn Lys Gln Val		
130	135	140
Leu Asp Leu Glu Ala Gly Phe Gly Ala Phe Tyr Ala Asn Tyr Ser Pro		
145	150	155 160
Lys Val Leu Pro Ser Ile Ala Ser Tyr Ser Trp Leu Leu Asp Gln Gln		
165	170	175
Asp Val Ala Phe Lys Arg Phe Pro Ala His Leu Ser Thr His Trp Val		
180	185	190
Ala Asp Ala Ala Ala Ser Val Arg Lys His Leu Val Ala Glu Arg Ala		
195	200	205
Leu Leu Pro Thr Asp Tyr Ile Lys Arg Ile Val Leu Arg Ile Pro Asn		
210	215	220

Val Gln Tyr Val Asn Arg Pro Phe Pro Val Ser Glu His Glu Ala Arg
 225 230 235 240

His Ser Phe Gln Tyr Val Ala Cys Ala Met Leu Leu Asp Gly Gly Ile
 245 250 255

Thr Val Pro Ser Phe His Glu Cys Gln Ile Asn Arg Pro Gln Val Arg
 260 265 270

Glu Leu Leu Ser Lys Val Glu Leu Glu Tyr Pro Pro Asp Asn Leu Pro
 275 280 285

Ser Phe Asn Ile Leu Tyr Cys Glu Ile Ser Val Thr Leu Lys Asp Gly
 290 295 300

Ala Thr Phe Thr Asp Arg Ser Asp Thr Phe Tyr Gly His Trp Arg Lys
 305 310 315 320

Pro Leu Ser Gln Glu Asp Leu Glu Glu Lys Phe Arg Ala Asn Ala Ser
 325 330 335

Lys Met Leu Ser Trp Asp Thr Val Glu Ser Leu Ile Lys Ile Val Lys
 340 345 350

Asn Leu Glu Asp Leu Glu Asp Cys Ser Val Leu Thr Thr Leu Leu Lys
 355 360 365

Gly Pro Ser Pro Pro Glu Val Ala Ser Asn Ser Pro Ala Cys Asn Asn
 370 375 380

Ser Ile Thr Asn Leu Ser
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<210> 5

<211> 652

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (56)..(307)

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Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val
           5                10                15

gtg ttc atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat 154
Val Phe Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr
           20                25                30

tct ctt tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa 202
Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu
           35                40                45

cct tgg gaa act gtg gac cct act gta cct caa aag ctt ata aca atc 250
Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile
           50                55                60                65

aac caa caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg 298
Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val
           70                75                80

acc aaa tgacgagccc tcgcctcttt ctctctgaaga gtactctata aatctagtgg 354
Thr Lys

aaacatttct gcacaaacta gattctggac accagtgtgc ggaaatgctt ctgctacatt 414

tttagggttt gtctacattt tttagggctct ggataaggaa ttaaaggagt gcagcaataa 474

ctgcactgtc taaaagtttg tgcttatctt ctgttaaatt tgaatattgc atattgaaat 534

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tctttaataa aatgccattt gtgcaagatt tctcaaagaa aaaaaaaaaa aaaaaaaaaa 652

<210> 6

<211> 83

<212> PRT

<213> Homo sapiens

<400> 6

Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu
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Val Val Phe Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val
20 25 30

Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
35 40 45

Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr
50 55 60

Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg
65 70 75 80

Val Thr Lys

<210> 7

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: NLG-2 forward
primer

<400> 7

cacggatcca ttcttcgctg aagtcacat gagg

34

<210> 8

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: NLG-2 reverse primer

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gtggaattct ttggcaccc ttggacatt ttgc

34

<210> 9

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: NLG-1-1 forward primer

<400> 9

cacggatcct tctttacaac gaaatgatgc tcaag

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<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: NLG-1-1 reverse

primer

<400> 10

gtggaattcg gagagatttg tgatagaatt attacatgc

39